



SEQUENCE LISTING

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Auge, Jennifer Stoehr
Ohlendorf, Douglas

<120> MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE

<130> 600.346USWO

<140> US 09/308,830
<141> 1999-08-04

<150> PCT/US97/22228
<151> 1997-12-05

<150> US 60/032,930
<151> 1996-12-06

<160> 14

<170> PatentIn version 3.1

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| atttgatata gtctaattcc accatcactt cttccactct ctctaccgtc acaacttcat | 480 |
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| tcgctactgt gtcacctaaa atatacccct tatcaatcgc ttcttttaaac tcatctatat | 600 |
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| | Met Glu Asn |
| | 1 |
| aat aaa aaa gta ttg aag aaa atg gta ttt ttt gtt tta gtg aca ttt | 884 |
| Asn Lys Lys Val Leu Lys Lys Met Val Phe Phe Val Leu Val Thr Phe | |
| 5 10 15 | |
| ctt gga cta aca atc tcg caa gag gta ttt gct caa caa gac ccc gat | 932 |
| Leu Gly Leu Thr Ile Ser Gln Glu Val Phe Ala Gln Gln Asp Pro Asp | |
| 20 25 30 35 | |
| cca agc caa ctt cac aga tct agt tta gtt aaa aac ctt caa aat ata | 980 |
| Pro Ser Gln Leu His Arg Ser Ser Leu Val Lys Asn Leu Gln Asn Ile | |
| 40 45 50 | |
| tat ttt ctt tat gag ggt gac cct gtt act cac gag aat gtg aaa tct | 1028 |
| Tyr Phe Leu Tyr Glu Gly Asp Pro Val Thr His Glu Asn Val Lys Ser | |
| 55 60 65 | |
| gtt gat caa ctt tta tct cac cat tta ata tat aat gtt tca ggg cca | 1076 |
| Val Asp Gln Leu Leu Ser His His Leu Ile Tyr Asn Val Ser Gly Pro | |
| 70 75 80 | |
| aat tat gat aaa tta aaa act gaa ctt aag aac caa gag atg gca act | 1124 |
| Asn Tyr Asp Lys Leu Lys Thr Glu Leu Lys Asn Gln Glu Met Ala Thr | |
| 85 90 95 | |
| tta ttt aag gat aaa aac gtt gat att tat ggt gta gaa tat tac cat | 1172 |
| Leu Phe Lys Asp Lys Asn Val Asp Ile Tyr Gly Val Glu Tyr Tyr His | |
| 100 105 110 115 | |
| ctc tgt tat tta tgt gaa aat gca gaa agg agt gca tgt atc tac gga | 1220 |
| Leu Cys Tyr Leu Cys Glu Asn Ala Glu Arg Ser Ala Cys Ile Tyr Gly | |
| 120 125 130 | |
| ggg gta aca aat cat gaa ggg aat cat tta gaa att cct aaa aag ata | 1268 |
| Gly Val Thr Asn His Glu Gly Asn His Leu Glu Ile Pro Lys Lys Ile | |
| 135 140 145 | |
| gtc gtt aaa gta tca atc gat ggt atc caa agc cta tca ttt gat att | 1316 |
| Val Val Lys Val Ser Ile Asp Gly Ile Gln Ser Leu Ser Phe Asp Ile | |
| 150 155 160 | |
| gaa aca aat aaa aaa atg gta act gct caa gaa tta gac tat aaa gtt | 1364 |
| Glu Thr Asn Lys Lys Met Val Thr Ala Gln Glu Leu Asp Tyr Lys Val | |
| 165 170 175 | |

| | |
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| aga aaa tat ctt aca gat aat aag caa cta tat act aat gga cct tct | 1412 |
| Arg Lys Tyr Leu Thr Asp Asn Lys Gln Leu Tyr Thr Asn Gly Pro Ser | |
| 180 185 190 195 | |
| | |
| aaa tat gaa act gga tat ata aag ttc ata cct aag aat aaa gaa agt | 1460 |
| Lys Tyr Glu Thr Gly Tyr Ile Lys Phe Ile Pro Lys Asn Lys Glu Ser | |
| 200 205 210 | |
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| ttt tgg ttt gat ttt ttc cct gaa cca gaa ttt act caa tct aaa tat | 1508 |
| Phe Trp Phe Asp Phe Phe Pro Glu Pro Glu Phe Thr Gln Ser Lys Tyr | |
| 215 220 225 | |
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| ctt atg ata tat aaa gat aat gaa acg ctt gac tca aac aca agc caa | 1556 |
| Leu Met Ile Tyr Lys Asp Asn Glu Thr Leu Asp Ser Asn Thr Ser Gln | |
| 230 235 240 | |
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| att gaa gtc tac cta aca acc aag taactttttg cttttggcaa ccttacctac | 1610 |
| Ile Glu Val Tyr Leu Thr Thr Lys | |
| 245 250 | |
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| tgctggattt agaaatttta ttgcaattct tttattaatg taaaaaccgc tcatttgatg | 1670 |
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| agcggtttttg tcttatctaa aggagcttta cctcctaattg ctgcaaaatt ttaaagtgtg | 1730 |
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| gattttttgta tttgtctatt gtatttgatg ggtaatccca tttttcgaca gacatcgtcg | 1790 |
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| |
|---|
| Asp Pro Asp Pro Ser Gln Leu His Arg Ser Ser Leu Val Lys Asn Leu |
| 35 40 45 |

| |
|---|
| Gln Asn Ile Tyr Phe Leu Tyr Glu Gly Asp Pro Val Thr His Glu Asn |
| 50 55 60 |

| |
|---|
| Val Lys Ser Val Asp Gln Leu Leu Ser His His Leu Ile Tyr Asn Val |
| 65 70 75 80 |

| |
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| Ser Gly Pro Asn Tyr Asp Lys Leu Lys Thr Glu Leu Lys Asn Gln Glu |
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85

90

95

Met Ala Thr Leu Phe Lys Asp Lys Asn Val Asp Ile Tyr Gly Val Glu
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Tyr Tyr His Leu Cys Tyr Leu Cys Glu Asn Ala Glu Arg Ser Ala Cys
115 120 125

Ile Tyr Gly Gly Val Thr Asn His Glu Gly Asn His Leu Glu Ile Pro
130 135 140

Lys Lys Ile Val Val Lys Val Ser Ile Asp Gly Ile Gln Ser Leu Ser
145 150 155 160

Phe Asp Ile Glu Thr Asn Lys Lys Met Val Thr Ala Gln Glu Leu Asp
165 170 175

Tyr Lys Val Arg Lys Tyr Leu Thr Asp Asn Lys Gln Leu Tyr Thr Asn
180 185 190

Gly Pro Ser Lys Tyr Glu Thr Gly Tyr Ile Lys Phe Ile Pro Lys Asn
195 200 205

Lys Glu Ser Phe Trp Phe Asp Phe Phe Pro Glu Pro Glu Phe Thr Gln
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35 40 45

Asn Val Ser Gly Pro Asn Tyr Asp Lys Leu Lys Thr Glu Leu Lys Asn
50 55 60

Gln Glu Met Ala Thr Leu Phe Lys Asp Lys Asn Val Asp Ile Tyr Gly
65 70 75 80

Val Glu Tyr Tyr His Leu Cys Tyr Leu Cys Glu Asn Ala Glu Arg Ser
85 90 95

Ala Cys Ile Tyr Gly Gly Val Thr Asn His Glu Gly Asn His Leu Glu
100 105 110

Ile Pro Lys Lys Ile Val Val Lys Val Ser Ile Asp Gly Ile Gln Ser
115 120 125

Leu Ser Phe Asp Ile Glu Thr Asn Lys Lys Met Val Thr Ala Gln Glu
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Leu Asp Tyr Lys Val Arg Lys Tyr Leu Thr Asp Asn Lys Gln Leu Tyr
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Thr Asn Gly Pro Ser Lys Tyr Glu Thr Gly Tyr Ile Lys Phe Ile Pro
165 170 175

Lys Asn Lys Glu Ser Phe Trp Phe Asp Phe Phe Pro Glu Pro Glu Phe
180 185 190

Thr Gln Ser Lys Tyr Leu Met Ile Tyr Lys Asp Asn Glu Thr Leu Asp
195 200 205

Ser Asn Thr Ser Gln Ile Glu Val Tyr Leu Thr Thr Lys
210 215 220